



UID: METH1 - 950aa Type: Protein 950 aa
METH1 - 950aa (SEQ ID NO:2)
vs.
UID: US 6649377 Type: Protein 949 aa
US 6649377

Local similarity
Match: 19
Mismatch: -17
Indel start: -13
Indel extend: -7

Score: 17959 at (METH1 - 950aa) [2..950] : (US 6649377) [1..949]

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2  GNAERAPGSRSGFPVPTLLLLAAALLAVSDALGRPSEEEDEELVVPELERAPGHGTTTLRL
  |||
1  GNAERAPGSRSGFPVPTLLLLAAALLAVSDALGRPSEEEDEELVVPELERAPGHGTTTLRL

62  HAFDQQLDLELRPDSSFLAPGFTLQNVGRKSGSETPLPETDLAHCIFYSGTVNGDPSSAAA
  |||
61  HAFDQQLDLELRPDSSFLAPGFTLQNVGRKSGSETPLPETDLAHCIFYSGTVNGDPSSAAA

122  LSLCEGVRGAFYLLGEAYFIQPLPAASERLATAAPGEKPPAPLQFHLLRRNRQGDVGGTC
  |||
121  LSLCEGVRGAFYLLGEAYFIQPLPAASERLATAAPGEKPPAPLQFHLLRRNRQGDVGGTC

182  GVVDDEPRPTGKAETEDDEGTEGEDEGEQWSPQDPALQGVGQPTGTGSIRKKRFVSSH
  |||
181  GVVDDEPRPTGKAETEDDEGTEGEDEGAQWSPQDPALQGVGQPTGTGSIRKKRFVSSH

242  YVETMLVADQSMAEFHGSGLKHYLLTLFSAARLYKHPSIRNSVSLVVVKILVIHDEQKG
  |||
241  YVETMLVADQSMAEFHGSGLKHYLLTLFSAARLYKHPSIRNSVSLVVVKILVIHDEQKG

302  PEVTSNAALTLRNFCNWQKQHNPSPDRDAEHYDTAILFTRQDLCGSQTCDTLGMADVGT
  |||
301  PEVTSNAALTLRNFCNWQKQHNPSPDRDAEHYDTAILFTRQDLCGSQTCDTLGMADVGT

362  CDPSRSCSVIEDDGLQAAFTTAHELGHVFNMPHDDAKQCASLNGVNQDSHMMASMLSNLD
  |||
361  CDPSRSCSVIEDDGLQAAFTTAHELGHVFNMPHDDAKQCASLNGVNQDSHMMASMLSNLD

422  HSQPWSPCSAYMITSFLDNHGHECLMDKPQNPIQLPGDLPGTSYDANRQCQFTFGEDSKH
  |||
421  HSQPWSPCSAYMITSFLDNHGHECLMDKPQNPIQLPGDLPGTSYDANRQCQFTFGEDSKH

482  CPDAASTCSTLWCTGTSGGVLCQTKHFPWADGTSCGEGKWCINGKCVNKTRKHFDTPF
  |||
481  CPDAASTCSTLWCTGTSGGVLCQTKHFPWADGTSCGEGKWCINGKCVNKTRKHFDTPF

542  HGSWGMWGPWGDCSRTCGGGVQYTMRECDNPVPKNGGKYCEGKRVRYRSCNLEDCPDNNG
  |||
541  HGSWGMWGPWGDCSRTCGGGVQYTMRECDNPVPKNGGKYCEGKRVRYRSCNLEDCPDNNG

602  KTFREEQCEAHNEFSKASFGSGPAVEWIPKYAGVSPKDRCKLICQAKGIGYFFVLQPKVV
  |||
601  KTFREEQCEAHNEFSKASFGSGPAVEWIPKYAGVSPKDRCKLICQAKGIGYFFVLQPKVV
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662 DGTPCSPDSTSVCVQGQCVKAGCDRIIDSKKKFDKCGVCGGNGSTCKKISGSVTSAPGY
 ||||||||||||||||||
 661 DGTPCSPDSTSVCVQGQCVKAGCDRIIDSKKKFDKCGVCGGNGSTCKKISGSVTSAPGY
 ||||||||||||||||||
 722 HDIITIPTGATNIEVKQRNQGRSRNNGSFLAIKAADGTYILNGDYTLSTLEQDIMYKGVV
 ||||||||||||||||||
 721 HDIITIPTGATNIEVKQRNQGRSRNNGSFLAIKAADGTYILNGDYTLSTLEQDIMYKGVV
 ||||||||||||||||||
 782 LRYSGSSAALERIRSFSPLEPLTIQVLTVGNALRPKIKYTYFVKKKKESFNAIPTFSAW
 ||||||||||||||||||
 781 LRYSGSSAALERIRSFSPLEPLTIQVLTVGNALRPKIKYTYFVKKKKESFNAIPTFSAW
 ||||||||||||||||||
 842 VIEEWGECSKSCELGWQRRLVECRDINGQPASECAKEVKPASTRPCADHPCPQWQLGEWS
 ||||||||||||||||||
 841 VIEEWGECSKSCELGWQRRLVECRDINGQPASECAKEVKPASTRPCADHPCPQWQLGEWS
 ||||||||||||||||||
 902 SCSKTCGKGYKKRSLKCLSHDGGVLSHESCDPLKKPKHFIDFCTMAECS
 ||||||||||||||||||
 901 SCSKTCGKGYKKRSLKCLSHDGGVLSHESCDPLKKPKHFIDFCTMAECS
 ||||||||||||||||||

Percent Identity: 99.7
 Percent Similarity: 99.8

UID: METH2 Type: Protein 890 aa
METH2 (SEQ ID NO:4)
vs.
UID: US 6649377 Type: Protein 949 aa
US 6649377

Local similarity

Match: 19
Mismatch: -17
Indel start: -13
Indel extend: -7

Score: 3038 at (METH2) [20..882] : (US 6649377) [18..880]

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20 LLLPLARGAPARPA---AGGQAS----ELVVP--TRLPGSAG--ELALHLSAF-----GK
   ||| || | | | | | | | | | | | | | | | | | | | | | | | |
18 LLL-LA--A-ALLAVSDALGRPSEDEELVVPPELERAPG-HGTTRLRLH--AFDQQLD--

64 GFVLR LAPDDSFLAPEFKIERL---G-GSGRAT-GGERGLRGCFSGTVNGEPESLAAVS
   | | | | | | | | | | | | | | | | | | | | | | | | | |
68 ---LELRPDSSFLAPGF---TLQNVGRKSGSETPLPETDLAHC FYSGTVNGDPSSAAALS

119 LCRGLSGSF-LLDGE-EFTIQPQGAGGS--L--AQPHRLQRWG---PAGARPL-----
   || | | | | | | | | | | | | | | | | | | | | | | | |
123 LCEGVRGAFYLL-GEAYF-IQPLPA-ASERLATAAP-----GEKPPA---PLQFHLLRR

163 PR-----GPEWEV---E---TG--EGQRQERGDHQEDSEEEESQEEEAEGA--SEPP-
   | | | | | | | | | | | | | | | | | | | | | | | | | |
171 NRQGDVG GTCG----VVDDEPRPTGKAE---TE--D--ED---EGTEGEDEGAQWS--PQ

203 -P-----PLGAT-S-RTKR FVSEARFVETLLVADASMAAFY GADLQNH-ILTLMSVAA
   | | | | | | | | | | | | | | | | | | | | | | | | | |
215 DPALQGVGQPTG-TGSIRKKRFVSSHRYVETMLVADQSMAEFHGSGL-KHYLLTLFSVAA

253 RIYKHPSIKNSINLMVVKVL-IVEDE-KWGPEV-SDNGGLTLRNFCNWQRRFNQPSDRHP
   | | | | | | | | | | | | | | | | | | | | | | | | | |
273 RLYKHPSIRNSVSLVVVKILVI-HDEQK-GPEVTS-NAALTLRNFCNWQKQHNPSPDRDA

310 EHYDTAILLTRQNFCG-QEGLCDTLGVADIGTICDPNKSCSVIEDEGLQAAHTLAHELGH
   || | | | | | | | | | | | | | | | | | | | | | | | |
330 EHYDTAILFTRQDLCSQ--TCDTLGMADVGTVC DPSRSCSVIEDDGLQAAFTTAHELGH

369 VLSMPHDDSKPCTRLFGPMGKHHV-----MA-PLFVHLN----QTLPWSPCSA-MYLTE
   | | | | | | | | | | | | | | | | | | | | | | | | | |
388 VFNMPHDDAKQCASLNG-----VNQDSHMMASML---SNLDHSQ--PWSPCSAYM-ITS

417 LLDGGHGDCLLDAPGAALP--LPTG-LPGRMALYQLD--QQCRQ-IFGPDFRHC PNTSAQ
   || | | | | | | | | | | | | | | | | | | | | | | | |
436 FLDNGHGECLMDKP--QNPIQLP-GDLPG--TSY--DANRQC-QFTFGEDSKHCP-----

471 D---VCAQLWC-HTDGAEPL-CHTKNGSLPWADGTPCGPGHLCSEGSCLP EEEV---ERP
   | | | | | | | | | | | | | | | | | | | | | | | | | |
483 DAASTCSTLWCTGTSG-GVLVCQTK--HFPWADGTSCGEGKWCINGKC-----VNKTHR-

523 K----PVVDGGWAPWGPWGECSRTCGGGVQF SHRECKD-PEPQNGGRYCLG-R-RAKYQS
   | | | | | | | | | | | | | | | | | | | | | | | | | |
534 KHFDTP-FHGSWGMWGPWGDCSRTCGGGVQYTMREC-DNPVPKNGGKYCEGKRVR--YRS
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